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GENOME ANNOUNCEMENT

Genome Sequence of the Persistent *Salmonella enterica* subsp. *enterica* Serotype Senftenberg Strain SS209

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***Salmonella enterica* subsp. *enterica* serotype Senftenberg is an emerging serotype in poultry production which has been found to persist in animals and the farm environment. We report the genome sequence and annotation of the SS209 strain of *S.* Senftenberg, isolated from a hatchery, which was identified as persistent in broiler chickens.**

Salmonelloses are a worldwide health problem and are usually associated with poultry products. Over the last decade, the emergence of some serotypes in poultry production has been observed (1, 14). *Salmonella enterica* serotype Senftenberg has always been associated with the hatchery environment, but recently it has become more frequent in poultry farms (7, 10). Furthermore, some strains were responsible for several human infections throughout the world (8, 11). In order to understand the emergence of the Senftenberg serotype in poultry, we previously identified a group of *S.* Senftenberg strains showing high intestinal colonization levels and able to persist over several weeks in broiler chickens, contrary to the case with other strains (2). The SS209 strain presented in this study is one of the persistent strains. It originated with 1-day-old chicks and belongs to the multilocus sequence type (MLST) ST14, the most common sequence type found in serotype Senftenberg worldwide (13).

Here we report the genome sequence of *S.* Senftenberg SS209, obtained using a combination of 454 pyrosequencing and Illumina genome analyzer IIx paired-end reads (performed by GATC Biotech, Konstanz, Germany). Sequencing yielded 239,453 reads for 454 sequencing (17.2-fold coverage) and 1,733,213 paired-end reads for Illumina (24.8-fold coverage), which were assembled *de novo* using the Newbler 2.3 assembly software program (Roche). The minimum contig size was set to 500 nucleotides (nt), which generated 109 contigs for the bacterial chromosome. No sequences corresponding to the large plasmid present in some *Salmonella* serotypes were detected. Genome annotation was performed using the AGMIAL annotation platform (3) and the *S.* Typhimurium strain LT2 as a reference (9).

The chromosome of *S.* Senftenberg SS209 has an overall G+C content of 51.73% and a predicted genome size of about 5.02 Mb, which is similar to the estimated genome length of the other sequenced *S.* Senftenberg strain (6). It is composed of 4,838 coding sequences (CDS). A pseudogenome of SS209 has been constructed by ordering contigs using the Mauve Contig Mover software program (12) and the LT2 strain genome as a reference. Genomic alignment between SS209 and other *Salmonella* serotypes was then performed using the Mauve genome aligner (5) and postprocessed for integration into the MOSAIC resource (4). A first analysis of whole-genome comparisons showed that *S.* Senftenberg SS209 is quite distant from the serotypes commonly found in poultry, namely, *Salmonella enterica* serotypes Typhimurium, Enteritidis, and Gallinarum. The core genome (i.e., backbone) common to *S.* Senftenberg SS209 and any of the three other serotypes ranges between 4.20 Mb (with *S.* Gallinarum 287/91), 4.24 Mb (with *S.* Enteritidis P125109), and 4.33 Mb (with *S.* Typhimurium LT2) and represents, respectively, 80.7% (*S.* Gallinarum), 81.4% (*S.* Enteritidis), and 83.1% (*S.* Typhimurium) of the SS209 genome. The aligned pairs of backbones share 98.8% of identity on average compared to any of the *S.* Gallinarum, *S.* Typhimurium, and *S.* Enteritidis genomes. Further genomic studies should allow a better understanding of *S.* Senftenberg evolution, especially the relationships between this emergent serotype and the other pathogenic *Salmonella* serotypes.

Nucleotide sequence accession number. The *S.* Senftenberg strain SS209 whole-genome sequence assembly and its annotation have been deposited in EMBL under the project accession number CAGQ00000000.

ACKNOWLEDGMENTS

Sequencing work was funded by the grant AIP Bio-Ressources from the Institut National de la Recherche Agronomique. Z.B. holds a doctoral fellowship from the French agency for food, environmental, and occupational health safety (Anses) and INRA.

We are grateful to the INRA MIGALE bioinformatics platform (http://migale.jouy.inra.fr) for providing computational resources.

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Received 17 February 2012 **Accepted** 24 February 2012

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doi:10.1128/JB.00255-12

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